

Fig. 1

PPSS-I

SEQ ID NO: 8 5'GGGGGGGGGAACAGGAGCAGCAGAGAACTCAAGAGAGAGCCAACTCTCAACGATTGTCTGCCCAATTGAACACCTTTATTC 81

ATCCTCTGCCTCCCCCGAGACCCAGAAGAAG ATG CTC TCG ACG CGT GTC CAG TGC GCC CTA GCA CTA CTC 152

SEQ ID NO: 3 Met Leu Ser Thr Arg Val Gln Cys Ala Leu Ala Leu Leu -88

TCC CTA GCC CTG GCC ATC AGC AGC GTC TCT GCC GCT CCG GAT GCC AAA CTC CGC CAG CTG 214

Ser Leu Ala Leu Ala Ile Ser Ser Val Ser Ala Ala Pro Ser Asp Ala Lys Leu Arg Gln Leu -67

CTC CAA CGG TCA CTC ATG GCA CCT GCA GGC AAA CAG GAG CTT GCC AGG AAT ACA CTC GTA GAG 272

Leu Gln Arg Ser Leu Met Ala Pro Ala Gly Lys Gln Glu Leu Ala Arg Asn Thr Leu Val Glu -46

CTA CTC TCA GAG CTC GCA CAT GTA GAG AAC GAG GCG ATT GAA TTG GAT GAC ATG TCT CAT GGC 340

Leu Leu Ser Glu Leu Ala His Val Glu Asn Glu Ala Ile Glu Leu Asp Asp Met Ser His Gly -25

GTG GAG CAG GAG GAT GTG GAT CTC GAG CTG GAG CGT GCA CCC GGC CCA GTA CTG GCT CCA CGT 403

Val Glu Gln Glu Asp Val Asp Leu Glu Leu Glu **Arg** Ala Pro Gly Pro Val Leu Ala Pro Arg -4

GAA CGC AAG GCT GGA TGC AAG AAC TTC TTC TGG AAG ACC TTT ACA TCG TGT TAA TGAATCTACTC 466

Glu **Arg** **lys** Ala Gly Cys Lys Asn Phe Phe Thr Lys Thr Ser Cys ***

CTTTACTGTGTACTACATCTCATCTCTTTTGTTCATCACTCATTTGCTGAATCCAATGCACCATGGCCTAACCCCTCT 549

TCAAAAAATTAAATAAACACTGTTATAACTTTAAACAATCAATCTGATGTTTCTATCGCTCACTTAGATTTTTCGAAAAAG 632

GAACACAAGAAAGAAATGTTCTACAAATGATGCGGTTCTGCTTTGACTGTGATTATGTATTTTGGCAGACTATTTTAAATTG 715

TTTGTTTGAATAAAATCTGTGTTTTCAGAACCAAAAAA 3'

Fig. 2

SEQ ID NO: 14	PPSS-II'	PPSS-II' and PPSS-II"										75
		accaggcctgctccataccgactgatccagatagcccggtccagctcagctcgtcaccgctgcca										70
SEQ ID NO: 20	PPSS-II"	accaggcctgctccataccgactgatccagatagcccggtccagctcagctcgtcaccgctgcca										139/-91
		accaggcctgctccataccgactgatccagatagcccggtccagctcagctcgtcaccgctgcca										134/-87
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCC CTG GCC										196/-72
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										191/-68
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										253/-53
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										248/-49
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										304/-35
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										305/-30
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										358/-18
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										350/-14
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										415/+2
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										398/+2
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										477
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										460
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										552
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										535
PPSS-II'	PPSS-II"	tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										552
		tccctgcaaaacccagctctgttgag ATG AAG GTC TGC CGA ATC CAC TGT GCA CTG GCC										535

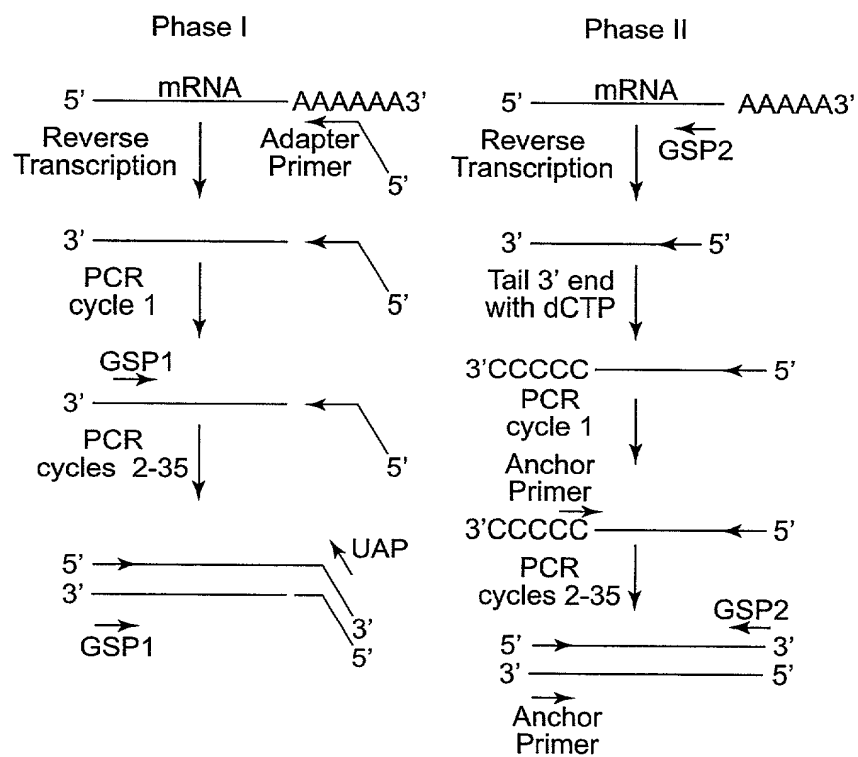


Fig. 4

Nucleotide Identity

TR1	82.8	49.0	43.7	52.3	51.0	52.0	51.5	51.1	52.8	54.5
84.1	TR1	48.2	39.1	44.9	50.0	50.0	49.5	48.0	49.8	52.5
45.5	43.9	TR1	58.1	77.0	67.7	68.9	67.9	69.4	69.4	72.5
35.6	35.6	52.3	AF1	60.1	58.8	55.1	53.8	55.3	56.8	56.8
44.7	40.9	73.5	52.3	CF1	65.7	68.7	67.7	68.4	67.7	72.2
47.7	44.7	70.5	49.2	64.4	FR1	75.0	74.5	62.6	75.5	78.3
42.4	38.6	66.7	46.2	63.6	78.8	C	84.1	84.3	84.3	84.3
42.4	38.6	65.2	45.5	62.9	78.0	87.9	R	92.4	91.2	92.2
42.4	38.6	66.7	46.2	63.6	78.8	88.6	97.0	B	94.4	95.5
42.4	38.6	64.4	46.2	62.9	78.8	90.9	96.2	98.5	M	98.7
45.5	42.4	73.5	47.7	68.2	87.1	91.7	97.7	98.5	100	H

Amino Acid Identity

Fig. 5

Comparison of Amino Acid Sequences of Peptides Derived from Preprosomatostatin Ia

	-20	-10	+1	+10	+14	SEQ ID NO:
Rainbow trout ^b						4
Hagfish ^d						27
Lamprey ^d						1
Torpedo ^d						1
Ratfish ^d						28
Bowfin ^d						29
Sturgeon ^d						30
Catfish ^d						1
Salmon ^d						1
Anglerfish ^c						31
Bel ^d						1
Flounder ^d						2
Sculpin ^d						1
Progc						1
Salamander ^d						1
Alligator ^d						1
Pigeon ^d						1
Ovined						32

Fig. 6

Sequence comparison

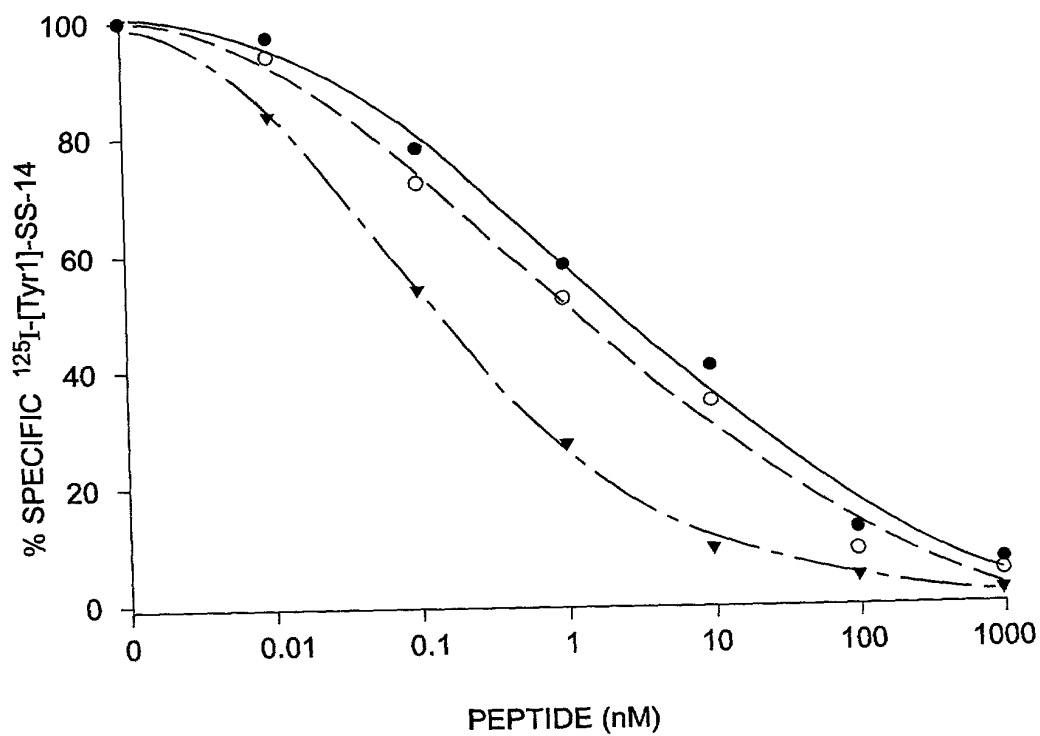
SEQ	ID NO:	TRII'
SEQ	9	TRII'
SEQ	15	TRII''
SEQ	36	CFII
SEQ	37	AFII
SEQ	38	GFII
SEQ	39	GFII1
SEQ	40	FRII
SEQ	3	TRI
SEQ	41	CFI
SEQ	42	AFI
SEQ	43	GFI
SEQ	44	FRI
SEQ	45	C
SEQ	46	R
SEQ	47	B
SEQ	48	M
SEQ	49	H

(continued)

(continued)

WRTFYPNCPCCLR--PRKVKCP-AGAKE-DLR--VELERSVGN-PNNLPPRPRKAGCKNFYWKGFJTSC
WRTFYPNCPCCLRWRPKVKGQPKAKE-DL-----ERSV-----DNLPPRPRKAGCKNFYWKGFJTSC
LPELQW-MLSNNELTPVQVEEAPRS-----RLEIVRDN-----T-VTSKPLNCWNYFWKSRJAC
VEELIAQMSLPEATFQREAEDASMATE-G-----RMNLESRVDS-TNNLPPRPRKAGCKNFYWKGFJTSC
VEKLSLSIPIEMEMR--EKGLSWAGE-SEDLRLQEERSAES-SNOLPTRVRKEGCKNFYWKGFJTSC
ISGLLD-GVDNSVLDGEIAPVPFAEEPLESRLE-ERAVYNRLSQLPQDRKAPCKNFYWKGFJTSC
LSGWTD-S-RESNLIEVERNVDPPE-P-----KIPPSVK--FPRLSRERKAGCKNFYWKGFJTSC
LVLELLS-ELAHVENAEIELDMWSHGE-QEDVDLELERAPG--PVLAPRERKAGCKNFYWKGFJTSC
LAEILA-ELAEAEENIELDSVEFSRAAE-SEGARLEMERAAAG--PMLAPRERKAGCKNFYWKGFJTSC
LAEILLSDLLQGENEALEEFENFLAEGGPEDAHDLERAASG-GPILAPRERKAGCKNFYWKGFJTSC
LADLLS-ELVQAENEALEPEDLSRAVE-KDEVPLELERAAG--PMLAPRERKAGCKNFYWKGFJTSC
LAEILS-EPQSQTDNEALESDDLPRGAE-QDEVRLLELERSANS-SPALAPRERKAGCKNFYWKGFJTSC
LAEILS-EPQSQTENEALSESIDLSPGAE-QDEVRLLELERSANS-NPALAPRERKAGCKNFYWKGFJTSC
LAEILS-EPNQNTENDALEPEDLPQAAE-QDEMRLLELQRSANS-NPAMAPRERKAGCKNFYWKGFJTSC
LAEILS-EPNQNTETIDALEPEDLSQAAE-QDEMRLLELQRSANS-NPAMAPRERKAGCKNFYWKGFJTSC
LAEILS-EPNQNTENDALEPEDLSQAAE-QDEMRLLELQRSANS-NPAMAPRERKAGCKNFYWKGFJTSC
LAEILS-EPNOTENDALEPEDLSQAAE-QDEMRLLELQRSANS-NPAMAPRERKAGCKNFYWKGFJTSC

Fig. 2

*Fig. 8*